

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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SEQUENCE LISTING

<110> LONGACRE-ANDRE, SHIRLEY
 ROTH, CHARLES
 NATO, FARIDABANO
 BARNWELL, JOHN
 MENDIS, KAMINI

<120> RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
 PLASMODIUM MSP-1

<130> 0660-0139-0XPCT

<140> 09/125,031

<141> 1999-03-10

<150> PCT/FR97/00290

<151> 1997-02-14

<150> FR96/01822

<151> 1996-02-14

<160> 14

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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aac	tct	ggc	tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	96
Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	
		20					25					30				

ctg	ctg	aac	tac	aaa	cag	gag	ggc	gac	aag	tgc	gtg	gag	aac	ccc	aac	144
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Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn		
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ccg	acc	tgt	aac	gag	aac	aac	ggc	ggc	tgt	gac	gca	gac	gcc	aaa	tgc	192	
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys		
	50					55					60						
acc	gag	gag	gac	tcg	ggc	agc	aac	ggc	aag	aaa	atc	acg	tgt	gag	tgt	240	
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys		
	65				70					75					80		
acc	aaa	ccc	gac	tcg	tac	ccg	ctg	ttc	gac	ggc	atc	ttc	tgc	agc	taa	288	
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taa																291	

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		20						25					30				
Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn		
		35					40					45					
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys		
	50					55				60							
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys		
	65				70				75						80		
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  1             5             10             15

aac tct ggc tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt 96
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys
      20             25             30

ctg ctg aac tac aaa cag gag ggc gac aag tgc gtg gag aac ccc aac 144
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
      35             40             45

ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc 192
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
      50             55             60

acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt 240
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
      65             70             75             80

acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc tcc 288
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser Ser
      85             90             95

tct aac ttc ttg ggc atc tcg ttc ttg ttg atc ctc atg ttg atc ttg 336
Ser Asn Phe Leu Gly Ile Ser Phe Leu Leu Ile Leu Met Leu Ile Leu
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Tyr Ser Phe Ile
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 35 40 45
 Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
 50 55 60
 Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
 65 70 75 80
 Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser Ser
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 tgtgttgaaa atccaaatcc tacttgtaac gaaaataatg gtggatgtga tgcagatgcc 180
 aaatgtaccg aagaagattc aggtagcaac ggaaagaaaa tcacatgtga atgtactaaa 240
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gaa ttc aac atc tcg cag cac caa tgc gtg aaa aaa caa tgt ccc gag	96
Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu	
20 25 30	
gaa ttc aac atc tcg cag cac caa tgc gtg aaa aaa caa tgt ccc gag	144
Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu	
35 40 45	
aac tct ggc tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt	192
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys	
50 55 60	
ctg ctg aac tac aaa cag gag ggc gac aag tgc gtg gag aac ccc aac	240
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn	
65 70 75 80	
ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc	288
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys	
85 90 95	
acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt	336
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys	
100 105 110	
acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc taa	384
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<212> PRT

<213> Plasmodium falciparum

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Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu	
35 40 45	

Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys
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Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys
				85					90					95	
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys
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<222> (1)..(330)

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Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	Cys	Pro	Glu	Asn	Ser	Gly	
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tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	ctg	ctg	aac	144
Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	Leu	Leu	Asn	
			35				40					45				
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Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn	Pro	Thr	Cys	
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aac	gag	aac	aac	ggc	ggc	tgt	gac	gca	gac	gcc	aaa	tgc	acc	gag	gag	240
Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys	Thr	Glu	Glu	
65				70						75					80	
gac	tcg	ggc	agc	aac	ggc	aag	aaa	atc	acg	tgt	gag	tgt	acc	aaa	ccc	288
Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys	Thr	Lys	Pro	
				85				90						95		
gac	tcg	tac	ccg	ctg	ttc	gac	ggc	atc	ttc	tgc	agc	taa	taa			330
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105

110

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 35 40 45
 Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn Pro Thr Cys
 50 55 60
 Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys Thr Glu Glu
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	50					55					60					
Arg	Asn	Tyr	Phe	Leu	Asp	Val	Leu	Asn	Ser	Asp	Leu	Asn	Pro	Tyr	Ser	
65					70					75					80	
Ile	Pro	His	Ser	Gly	Glu	Tyr	Ile	Ile	Lys	Asp	Pro	Tyr	Lys	Leu	Leu	
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	130					135					140					
Cys	Ile	Lys	Glu	Val	Glu	Ala	Asn	Ile	Asn	Lys	His	Asp	Glu	Glu	Ile	
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				245					250					255		
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			260					265					270			
Glu	Ser	Lys	Lys	Ala	Leu	Ser	Glu	Leu	Leu	Asn	Val	Gln	Thr	Gln	Met	
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Leu Leu Tyr Phe Lys Glu Asp Ala Gly Lys Cys Val Pro Ala Pro Asn				
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Met Thr Cys Lys Asp Lys Asn Gly Gly Cys Ala Pro Glu Ala Glu Cys				
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35 40 45
Ala Phe Asn Thr Asn Ile Thr Asp Met Leu Asp Ser Arg Leu Lys Lys
50 55 60
Arg Asn Tyr Phe Leu Glu Val Leu Asn Ser Asp Leu Asn Pro Phe Lys

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Ala	Ser	Ile	Asp	Lys	Asp	Leu	Ala	Thr	Ala	Asn	Asp	Gly	Val	Thr	Tyr	
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Tyr	Asn	Lys	Met	Gly	Glu	Leu	Tyr	Lys	Thr	His	Leu	Thr	Ala	Val	Asn	
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Glu	Glu	Val	Lys	Lys	Val	Glu	Ala	Asp	Ile	Lys	Ala	Glu	Asp	Asp	Lys	
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Ile	Lys	Lys	Ile	Gly	Ser	Asp	Ser	Thr	Lys	Thr	Thr	Glu	Lys	Thr	Gln	
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Ser	Met	Ala	Lys	Lys	Ala	Glu	Leu	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn	
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Ser	Leu	Gln	Lys	Glu	Tyr	Glu	Ser	Leu	Val	Ser	Lys	Val	Asn	Thr	Tyr	
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Thr	Asp	Asn	Leu	Lys	Lys	Val	Ile	Asn	Asn	Cys	Gln	Leu	Glu	Lys	Lys	
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225					230					235					240	
Glu	Lys	Leu	Glu	Glu	Tyr	Lys	Lys	Ser	Glu	Lys	Lys	Asn	Glu	Val	Lys	
				245					250					255		
Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Lys	Ser	Lys	Leu	Ile	Lys	Glu	
			260					265					270			
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Leu	Leu	Thr	Met	Ser	Ser	Glu	His	Thr	Cys	Ile	Asp	Thr	Asn	Val	Pro	
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Cys	Leu	Leu	Thr	Phe	Lys	Glu	Glu	Gly	Gly	Lys	Cys	Val	Pro	Ala	Ser	
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Asn	Val	Thr	Cys	Lys	Asp	Asn	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu
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Cys	Lys	Met	Thr	Asp	Ser	Asn	Lys	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu
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Ala	Gly	Met	Tyr	Lys	Thr	Ile	Lys	Lys	Gln	Leu	Glu	Asn	His	Val	Asn
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Arg	Asn	Tyr	Phe	Leu	Glu	Val	Leu	Asn	Ser	Asp	Leu	Asn	Pro	Phe	Lys
65					70					75					80
Tyr	Ser	Ser	Ser	Gly	Glu	Tyr	Ile	Ile	Lys	Asp	Pro	Tyr	Lys	Leu	Leu
				85					90					95	
Asp	Leu	Glu	Lys	Lys	Lys	Lys	Leu	Ile	Gly	Ser	Tyr	Lys	Tyr	Ile	Gly
			100					105					110		

Ala	Ser	Ile	Asp	Met	Asp	Leu	Ala	Thr	Ala	Asn	Asp	Gly	Val	Thr	Tyr	
		115					120					125				
Tyr	Asn	Lys	Met	Gly	Glu	Leu	Tyr	Lys	Thr	His	Leu	Asp	Gly	Val	Lys	
	130					135					140					
Thr	Glu	Ile	Lys	Lys	Val	Glu	Asp	Asp	Ile	Lys	Lys	Gln	Asp	Glu	Glu	
145					150					155					160	
Leu	Lys	Lys	Leu	Gly	Asn	Val	Asn	Ser	Gln	Asp	Ser	Lys	Lys	Asn	Glu	
				165					170					175		
Phe	Ile	Ala	Lys	Lys	Ala	Glu	Leu	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn	
			180					185					190			
Ser	Leu	Gln	Lys	Glu	Tyr	Glu	Ser	Leu	Val	Ser	Lys	Val	Asn	Thr	Tyr	
		195					200					205				
Thr	Asp	Asn	Leu	Lys	Lys	Val	Ile	Asn	Asn	Cys	Gln	Leu	Glu	Lys	Lys	
	210					215					220					
Glu	Ala	Glu	Ile	Thr	Val	Lys	Lys	Leu	Gln	Asp	Tyr	Asn	Lys	Met	Asp	
225					230					235					240	
Glu	Lys	Leu	Glu	Glu	Tyr	Lys	Lys	Ser	Glu	Lys	Lys	Asn	Glu	Val	Lys	
				245					250					255		
Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Lys	Ser	Lys	Leu	Ile	Lys	Glu	
			260					265					270			
Asn	Glu	Ser	Lys	Glu	Ile	Leu	Ser	Gln	Leu	Leu	Asn	Val	Gln	Thr	Gln	
		275					280					285				
Leu	Leu	Thr	Met	Ser	Ser	Glu	His	Thr	Cys	Ile	Asp	Thr	Asn	Val	Pro	
	290					295					300					
Asp	Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	Gly	Thr	Glu	Glu	Trp	Arg	
305					310					315					320	
Cys	Leu	Leu	Thr	Phe	Lys	Glu	Glu	Gly	Gly	Lys	Cys	Val	Pro	Ala	Ser	
				325					330					335		
Asn	Val	Thr	Cys	Lys	Asp	Asn	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu	
			340					345					350			
Cys	Lys	Met	Thr	Asp	Ser	Asn	Lys	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu	
		355					360					365				
Gly	Ser	Glu	Pro	Leu	Phe	Glu	Gly	Val	Phe	Cys	Ser					

370

375

380

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<211> 281

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:ALIGNMENT

<220>

<223> Amino Acids 1-115-REGION I

<220>

<223> Amino Acids 116-125-REGION II

<220>

<223> Amino Acids 126-197-REGION III

<220>

<223> Amino Acids 198-281-REGION IV

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Asp	Gln	Val	Thr	Thr	Gly	Glu	Ala	Glu	Ser	Glu	Ala	Pro	Glu	Ile	Val
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Pro	Gly	Ile	Tyr	Asp	Val	Val	Tyr	Lys	Pro	Leu	Ala	Gly	Met	Tyr	Lys
			20					25					30		

Thr	Ile	Lys	Lys	Leu	Glu	Asn	His	Val	Asn	Ala	Asn	Thr	Asn	Ile	Asp
		35					40					45			

Met	Leu	Asp	Ser	Ala	Leu	Lys	Lys	Ala	Asn	Tyr	Phe	Leu	Val	Leu	Asn
	50					55					60				

Ser	Asp	Leu	Asn	Pro	Ser	Gly	Glu	Tyr	Ile	Ile	Lys	Asp	Pro	Tyr	Lys
65					70					75					80

Leu	Leu	Asp	Leu	Glu	Lys	Lys	Lys	Leu	Gly	Ser	Tyr	Lys	Tyr	Ile	Gly
				85					90					95	

Ala	Ser	Asp	Asp	Thr	Ala	Asn	Asp	Gly	Tyr	Tyr	Lys	Met	Gly	Leu	Tyr
			100					105					110		

Lys	His	Leu	Val	Lys	Val	Glu	Ile	Asp	Lys	Lys	Gly	Lys	Ala	Lys	Lys
		115					120					125			

Glu	Leu	Lys	Tyr	Leu	Pro	Phe	Leu	Ser	Gln	Lys	Glu	Tyr	Leu	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130						135										140
Val	Tyr	Thr	Asp	Leu	Lys	Lys	Ile	Asn	Asn	Cys	Gln	Glu	Lys	Lys	Glu	
145					150					155					160	
Glu	Val	Lys	Leu	Asp	Tyr	Lys	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Lys	Val	
				165					170					175		
Lys	Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Ser	Lys	Leu	Ile	Glu	Ser	
			180					185					190			
Lys	Leu	Ser	Leu	Leu	Asn	Val	Gln	Thr	Gln	Leu	Met	Ser	Ser	Glu	His	
		195					200					205				
Cys	Ile	Asp	Thr	Asn	Val	Pro	Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	
	210					215					220					
Gly	Thr	Glu	Glu	Trp	Arg	Cys	Leu	Leu	Phe	Lys	Glu	Gly	Lys	Cys	Val	
225					230					235					240	
Pro	Ala	Asn	Thr	Cys	Lys	Asp	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu	
				245					250					255		
Cys	Lys	Met	Asp	Asn	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu	Gly	Ser	Glu	
			260					265					270			
Pro	Leu	Phe	Glu	Gly	Val	Phe	Cys	Ser								
		275					280									